SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Linemeyer, David L.
               Menke, John G.
               Hess, John F.
               Borkowski, Joseph A.
               Bierillo, Kathleen K.

   (ii) TITLE OF INVENTION: DNA ENCODING BRADYKININ B1 RECEPTOR

  (iii) NUMBER OF SEQUENCES: 2

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: John W. Wallen III
       (B) STREET: P.O. Box 2000
       (C) CITY: Rahway
       (D) STATE: New Jersey
       (E) COUNTRY: USA
       (F) ZIP: 07065

    (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE:
       (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Wallen III, John W.
       (B) REGISTRATION NUMBER: 35,403
       (C) REFERENCE/DOCKET NUMBER: 19202

   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: (908) 594-3905
       (B) TELEFAX: (908) 594-4720

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1307 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CAGAGAAAAC TCCTCCAAAA GCAGCTCTCA CTATCAGAAA ACCCAACTAC AGTTGTGAAC      60

GCCTTCATTT TCTGCCTGAG GTCTCAGTCC GTCGGCCCAG ACTGAAGTGC AGTGGCACAA     120

TCATAGCTCG CTGCAGCCTC GACCTTCCAG GCTTAAACGA TTCTCCCACC TCAGCCTCTC     180

GAGTTGCTGG GACCACAGGT CACTGTGCAT GGCATCATCC TGGCCCCCTC TAGAGCTCCA     240

ATCCTCCAAC CAGAGCCAGC TCTTCCCTCA AAATGCTACG GCCTGTGACA ATGCTCCAGA     300

AGCCTGGGAC CTGCTGCACA GAGTGCTGCC GACATTTATC ATCTCCATCT GTTTCTTCGG     360

CCTCCTAGGG AACCTTTTTG TCCTGTTGGT CTTCCTCCTG CCCCGGCGGC AACTGAACGT     420

GGCAGAAATC TACCTGGCCA ACCTGGCAGC CTCTGATCTG GTGTTTGTCT TGGGCTTGCC     480

CTTCTGGGCA GAGAATATCT GGAACCAGTT TAACTGGCCT TTCGGAGCCC TCCTCTGCCG     540

TGTCATCAAC GGGGTCATCA AGGCCAATTT GTTCATCAGC ATCTTCCTGG TGGTGGCCAT     600

CAGCCAGGAC CGCTACCGCG TGCTGGTGCA CCCTATGGCC AGCGGAAGGC AGCAGCGGCG     660

GAGGCAGGCC CGGGTCACCT GCGTGCTCAT CTGGGTTGTG GGGGGCCTCT TGAGCATCCC     720

CACATTCCTG CTGCGATCCA TCCAAGCCGT CCCAGATCTG AACATCACCG CCTGCATCCT     780

GCTCCTCCCC CATGAGGCCT GGCACTTTGC AAGGATTGTG GAGTTAAATA TTCTGGGTTT     840

CCTCCTACCA CTGGCTGCGA TCGTCTTCTT CAACTACCAC ATCCTGGCCT CCCTGCGAAC     900

GCGGGAGGAG GTCAGCAGGA CAAGGTGCGG GGGCCGCAAG GATAGCAAGA CCACAGCGCT     960

GATCCTCACG CTCGTGGTTG CCTTCCTGGT CTGCTGGGCC CCTTACCACT TCTTTGCCTT    1020

CCTGGAATTC TTATTCCAGG TGCAAGCAGT CCGAGGCTGC TTTTGGGAGG ACTTCATTGA    1080

CCTGGGCCTG CAATTGGCCA ACTTCTTTGC CTTCACTAAC AGCTCCCTGA ATCCAGTAAT    1140

TTATGTCTTT GTGGGCCGGC TCTTCAGGAC CAAGGTCTGG GAACTTTATA AACAATGCAC    1200

CCCTAAAAGT CTTGCTCCAA TATCTTCATC CCATAGGAAA GAAATCTTCC AACTTTTCTG    1260

GCGGAATTAA AACAGCATTG AACCAAGAAA AAAAAAAAAA AAAAAAA                  1307
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 353 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1               5                   10                  15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
            20              25                  30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
        35              40                  45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
    50              55                  60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
65              70                  75                  80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
            85                  90                  95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
            100             105                 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
            115             120                 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
    130             135                 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145             150                 155                 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
            165             170                 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
            180             185                 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
        195             200                 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
    210             215                 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Cys
225             230                 235                 240

Gly Gly Arg Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
            245             250                 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
            260             265                 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
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          275                 280                 285
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
    290                 295                 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305                 310                 315                 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
                325                 330                 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
            340                 345                 350

Asn
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